



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NATSUKA, SHUNJI
GERSTEN, KEVIN M.
LOWE, JOHN B.
- (ii) TITLE OF INVENTION: MURINE ALPHA (1,3) FUCOSYLTRANSFERASE
FUC-TVII, DNA ENCODING THE SAME, METHOD FOR PREPARING THE
SAME, ANTIBODIES RECOGNIZING THE SAME, IMMUNOASSAYS FOR
DETECTING THE SAME, PLASMIDS CONTAINING SUCH DNA
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
 - (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 - (C) CITY: ARLINGTON
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/613,098
 - (B) FILING DATE: 08-MAR-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: LAVALLEYE, JEAN-PAUL
 - (B) REGISTRATION NUMBER: 31,451
 - (C) REFERENCE/DOCKET NUMBER: 2363-114-55
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-413-3000
 - (B) TELEFAX: 703-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| ACAAACAGGA | AGGACAGCAG | GCTCTGGCAG | CCAGAAGCCT | GTGGCCCCAA | GCTGGCAGGA | 60 |
| TGGCCCCCTT | CCTGCAGGTC | CCCCACAGCC | TTCTGGGTTC | CTGACACGAG | AGAAGAGGTG | 120 |
| GGGCGGGGTG | AAGTGAAGTC | TGAAGCCAAA | ATGTGACTCT | CCTGGGGTCA | CCAGCTTGGG | 180 |
| GAGAGGTGAA | GAAAGATGCC | GGGGCGGAAA | CAAAGGGGCA | GATATCACTA | TGGTTATCTT | 240 |
| ACTAAGCACA | GAGTAACTGA | AAAAGCAAGG | GTACCGCTGC | CCACCTCGTG | CCCACCTTAC | 300 |
| GTTATACCTC | AAACCAGCTA | GATAGTTTCT | GATGGCACCC | ATACCCTCCC | TTCCCCTTTA | 360 |
| GGCATTGCGC | AAGCTCTCCA | CCACAATCTG | GAAGTTATAC | CCTGCGAGGG | GATGGGCAGG | 420 |
| GCACTTCTGA | GGTGCCAATC | AGCCTGCACT | CGCCTCTGCC | CTGGCCATGG | CACTGCTGTC | 480 |
| AGTTTCTTGG | TACCTGTCTC | AACAGCAGCC | TTGTCACGTG | AGACTATGGC | TGGCGGTGGG | 540 |
| GGTGGGGGCA | GGAATCCTAG | AAGCACAGGA | GTGACATAGG | GTCGGGTCGG | GCAGAGCGAA | 600 |
| GTGTAGGAGG | TGATCCCCAA | AGGGATGCTG | GGGACGATCT | GGCCAACACT | GTCCTCCCAT | 660 |
| TCAAACTCC | CAGTCTGGAG | CTCTGGGACA | TGGACAAGCC | AGGCCTGCTA | TTCTCCATAC | 720 |
| AGGGCTCCAT | AGTGTCTGGC | TCAGCAGAGT | GGGGGATCTG | GTGGGGATGG | AGGAAGCTTA | 780 |
| GCTAAAAGCT | TTGTATAGGC | TGAAGCTCTG | AGTGACCCTG | CTGGGCCACC | CTACCCTGGT | 840 |
| CTGGGCTGGG | TCATTGCATC | CCCAGATTGG | AAGGCTTGGT | GAGATGGAGA | GGAACCTTGG | 900 |
| CTACAAGCTA | TAGCTTTGCC | CACCAGAGCC | TGCTGGAGGG | GAATCAAACA | AGCCTGGACC | 960 |
| TGAGGCTGGG | ACTAGCTTTC | CTGTTTCTGG | AGTGGATGCC | AACCCCTGCG | CCACCAGCCT | 1020 |
| GCCTGTCCAC | GCCAGGGACA | CACAGACTCC | TTCCCTTTCC | AGACTGGAAA | GCCCCCTCCT | 1080 |
| GGGAGAGCAG | GAAGGAAGCA | ACCTGCAACT | CTTCCAGCCC | TGGACCTTGG | GCTGAACCTA | 1140 |
| CAGTTCAAGG | TTTGTATGCT | CACAGGTCTT | GGCAGGGAAA | GATAAGAATC | CCCAGGGCAC | 1200 |
| CCTCCCCCCC | GCCCCCAGT | CCACTGCAGG | TAGCTCCTGG | GTCTGCCCTT | CAGGGCAAGT | 1260 |
| GCTGACGCTC | CATCAGACTG | TGATGGGGCC | CTTTTCTGAG | GATGACAATT | CTGAGAACAA | 1320 |
| GGCATTTTTTC | TAGAGGTGGC | AGAACAGCAT | TTTGTGATGC | CCGAGGATCT | GGGAGCACAG | 1380 |
| GTCCAGCTTA | ATGAGGGATT | GGAGGAAGTG | GGTATCATCA | TTACAGGGAG | GGGCCTCTGT | 1440 |
| GGCCTCCTGG | GAAATGTCAG | TTGCTCTCTT | TGGGTGGCCT | GGGTTGTGT | GGTGGGCAGA | 1500 |
| GGACGGAGGT | GCTCATTTGG | GGAAGGGATC | ACTTCTGCTC | AGAGTGCTCG | CAAGGGCCTT | 1560 |
| TCCTTTTCCT | GAAGGCAAGC | AGGCCTCCTC | CTCCTCCTCT | TCCTCCTTCT | CCTCTTCCTC | 1620 |
| CTCTTTCTCC | ATATGCCTAG | CTGGTCATTT | CTAGGGACCA | GCATGGTTGG | GAAGGGGGCC | 1680 |

| | | | | | | |
|------------|--------------|------------|------------|------------|------------|------|
| TTGTCTTGGC | CTTCCTCTTG | TCTCAATTCC | CTCTTTGAGC | AGAAGACGGG | GTGGGTGGGG | 1740 |
| TAGGATTGGA | TAGTGGTTGA | TGCCAAAGAT | TGAAGGGGTA | GGGCGGGGCA | GAAGTGGGAA | 1800 |
| GGTCCCTGGC | TTCCTCACCT | TGGTAGATGG | TGAGGAGCCC | CAGAGGTTGA | GCTGAGCAGC | 1860 |
| AGCTGTGATT | TCAGGGTGCC | TCTGTTGGAG | AGGCTGCTGT | GATTTGAAAA | TCTTCTTTCC | 1920 |
| TTGGTGACAA | TTCCAGAAGG | CTCCAGATGA | ATTGTATTGG | TGAGTGCCTG | GCCCTTAAGC | 1980 |
| AGTCCCAGCT | GGGGATGATG | GGGATTTATG | GGTGTCCCTG | AGCCTAGGGT | GACAGGGCCT | 2040 |
| CTCCTTTTTT | TTTTATTCTG | CTTCAGGGTA | CCACCCACC | AGGAGGCTGC | GGGCCTGGGG | 2100 |
| CGGCCTAGCT | GGAGGAGCAA | CATTCATGGT | AATTTGGTTT | TTCTGGCTGT | GGGGATCAGC | 2160 |
| TCCTGGAAGT | GCCCCTGTGC | CTCAGTCCAC | ACTCACCATC | CTTATCTGGC | ACTGGCCTTT | 2220 |
| CACCAACCGG | CCGCCAGAGC | TACCTGGTGA | CACCTGCACT | CGCTATGGCA | TGGCCAGCTG | 2280 |
| CCGTCTGAGT | GCTAACCGGA | GCCTGCTAGC | CAGTGCTGAT | GCTGTGGTCT | TCCACCACCG | 2340 |
| TGAGCTGCAA | ACCCGGCAAT | CTCTCCTACC | CCTGGACCAG | AGGCCACACG | GACAGCCTTG | 2400 |
| GGTCTGGGCC | TCCATGGAAT | CGCCCAGTAA | TACCCATGGT | CTCCATCGCT | TCCGGGGCAT | 2460 |
| CTTCAACTGG | GTGCTGAGCT | ATCGGCGTGA | TTCAGATATC | TTTGTACCCT | ACGGTCGCTT | 2520 |
| GGAGCCTCTC | TCTGGGCCCA | CATCCCCACT | ACCGGCCAAA | AGCAGGATGG | CTGCCTGGGT | 2580 |
| GATCAGCAAT | TTCCAGGAGC | GGCAGCAGCG | TGCAAAGCTG | TACCGGCAGC | TGGCCCCTCA | 2640 |
| TCTGCAGGTG | GATGTGTTCG | GTCGCGCCAG | CGGACGGCCC | CTATGCGCTA | ATTGTCTGCT | 2700 |
| GCCCACTTTG | GCCC GG TACC | GCTTCTACCT | GGCCTTTGAG | AACTCACAGC | ATCGGGACTA | 2760 |
| CATCACTGAG | AAGTTCTGGC | GCAATGCCCT | GGCGGCTGGT | GCTGTACCCG | TGGCGCTGGG | 2820 |
| ACCTCCTCGG | GCCACCTACG | AGGCTTTTGT | GCCACCAGAT | GCCTTTGTAC | ACGTGGACGA | 2880 |
| CTTCAGCTCT | GCCCGTGAAC | TGGCTGTCTT | CCTCGTCAGC | ATGAATGAGA | GTCGTTATCG | 2940 |
| TGGCTTCTTT | GCTTGGCGAG | ACCGGCTCCG | TGTGCGGCTC | CTGGGTGACT | GGAGGGAGCG | 3000 |
| CTTCTGCACC | ATCTGTGCCC | GCTACCCTTA | CTTGCCCCGC | AGCCAGGTCT | ATGAAGACCT | 3060 |
| TGAAAGCTGG | TTCCAGGCTT | GAATCCTGC | TGCTGGGAGA | GGCTGGATGG | GTGGGAGACT | 3120 |
| GATGTTGAAA | CCAAAGAGCT | GGGCATCCAG | GCTTTTGGTC | ACCATGGCAC | TACCCCAAGG | 3180 |
| CTTTTCCTGT | TCAGTGAGCA | GGAATTCAGG | ATATAAGGAG | AAGACTGGGC | TGAGATACCC | 3240 |
| TGGTGGGCTT | TAGAGTAGGG | GCCCAGGATA | AGAGACAATG | AATTAATGAG | GAGCATATGG | 3300 |
| GGAAGGTGGC | TGAGGGTCCC | TGACTTACCT | TGACCCATGG | CTGAAGGCTC | CATGCCCATG | 3360 |
| GCTGGAGCTG | GGACCCTACA | CTTCTATAGT | CAAGGTGCTT | AGCCTCAAGG | TTGCAGATGC | 3420 |

ACCCTCTAGT ACTCTGGGTG CAGACTGTAC ACTGGGCGCA GGGGGTTGTG GAAGGACAGT 3480
 GCAGATGATT CTGGGCTTTT GACACCACAG TTCCCCCAGG GAAAGAGGCA CTACTAATAA 3540
 AAACACTGAC AGAAATCTCC TGGTCAAGTC TGTTAGGCAG CAGAGCTCGA ATTC 3594

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Thr | Pro | Cys | Pro | Pro | Ala | Cys | Leu | Ser | Thr | Pro | Gly | Thr | His | 1 | 5 | 10 | 15 |
| Arg | Leu | Leu | Pro | Phe | Pro | Asp | Trp | Lys | Ala | Pro | Ser | Trp | Glu | Ser | Arg | 20 | 25 | 30 | |
| Lys | Glu | Ala | Thr | Cys | Asn | Ser | Ser | Ser | Pro | Gly | Pro | Trp | Ala | Glu | Pro | 35 | 40 | 45 | |
| Thr | Val | Gln | Met | Asn | Cys | Ile | Gly | Tyr | His | Pro | Thr | Arg | Arg | Leu | Arg | 50 | 55 | 60 | |
| Ala | Trp | Gly | Gly | Leu | Ala | Gly | Gly | Ala | Thr | Phe | Met | Val | Ile | Trp | Phe | 65 | 70 | 75 | 80 |
| Phe | Trp | Leu | Trp | Gly | Ser | Ala | Pro | Gly | Ser | Ala | Pro | Val | Pro | Gln | Ser | 85 | 90 | 95 | |
| Thr | Leu | Thr | Ile | Leu | Ile | Trp | His | Trp | Pro | Phe | Thr | Asn | Arg | Pro | Pro | 100 | 105 | 110 | |
| Glu | Leu | Pro | Gly | Asp | Thr | Cys | Thr | Arg | Tyr | Gly | Met | Ala | Ser | Cys | Arg | 115 | 120 | 125 | |
| Leu | Ser | Ala | Asn | Arg | Ser | Leu | Leu | Ala | Ser | Ala | Asp | Ala | Val | Val | Phe | 130 | 135 | 140 | |
| His | His | Arg | Glu | Leu | Gln | Thr | Arg | Gln | Ser | Leu | Leu | Pro | Leu | Asp | Gln | 145 | 150 | 155 | 160 |
| Arg | Pro | His | Gly | Gln | Pro | Trp | Val | Trp | Ala | Ser | Met | Glu | Ser | Pro | Ser | 165 | 170 | 175 | |
| Asn | Thr | His | Gly | Leu | His | Arg | Phe | Arg | Gly | Ile | Phe | Asn | Trp | Val | Leu | 180 | 185 | 190 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Arg | Arg | Asp | Ser | Asp | Ile | Phe | Val | Pro | Tyr | Gly | Arg | Leu | Glu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Leu | Ser | Gly | Pro | Thr | Ser | Pro | Leu | Pro | Ala | Lys | Ser | Arg | Met | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Trp | Val | Ile | Ser | Asn | Phe | Gln | Glu | Arg | Gln | Gln | Arg | Ala | Lys | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Tyr | Arg | Gln | Leu | Ala | Pro | His | Leu | Gln | Val | Asp | Val | Phe | Gly | Arg | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ser | Gly | Arg | Pro | Leu | Cys | Ala | Asn | Cys | Leu | Leu | Pro | Thr | Leu | Ala | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Tyr | Arg | Phe | Tyr | Leu | Ala | Phe | Glu | Asn | Ser | Gln | His | Arg | Asp | Tyr | Ile |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Thr | Glu | Lys | Phe | Trp | Arg | Asn | Ala | Leu | Ala | Ala | Gly | Ala | Val | Pro | Val |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ala | Leu | Gly | Pro | Pro | Arg | Ala | Thr | Tyr | Glu | Ala | Phe | Val | Pro | Pro | Asp |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ala | Phe | Val | His | Val | Asp | Asp | Phe | Ser | Ser | Ala | Arg | Glu | Leu | Ala | Val |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Phe | Leu | Val | Ser | Met | Asn | Glu | Ser | Arg | Tyr | Arg | Gly | Phe | Phe | Ala | Trp |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Arg | Asp | Arg | Leu | Arg | Val | Arg | Leu | Leu | Gly | Asp | Trp | Arg | Glu | Arg | Phe |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Cys | Thr | Ile | Cys | Ala | Arg | Tyr | Pro | Tyr | Leu | Pro | Arg | Ser | Gln | Val | Tyr |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Glu | Asp | Leu | Glu | Ser | Trp | Phe | Gln | Ala | | | | | | | |
| 385 | | | | | 390 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "SYNTHETIC PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGGATCC CACCATCCTT ATCTGGCACT GGCCTTTCAC C

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCGGATCC AGTTCAAGCC TGGAACCAGC TTTCAAGGTC CTTC